SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT:
 - (A) NAME: Max-Planck-Gosellschaft zur Foerderung der Wissenschaften e.V.
 - (B) STREET: none
 - (C) CITY: Berlin
 - (E) COUNTRY: DE
 - (F) POSTAL CODE (ZIP): none
 - (ii) TTTLE OF INVENTION: Nucleic acid molecules encoding an RNA-directed RNA polymerase (RdRP)
 - (iii) NUMBER OF SEQUENCES: 2
 - (iv) COMPUTER READABLE FORM:

 (A) MEDIUM TYPE: Floppy disk

 (B) COMPUTER IBM PC compatible

 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (vi) ORIGINAL SOURCE:
 - (A) OR ANISM: Tomato

 - (ix) FEATURE: (A) NAME/KEY: CDS
 - (B) LOCATION:194..3535
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAAATATTCT TTACTTACTT CACCAGGGAT TGACTGATCA CTCCCCTCAA GTCTTTGTGT 60

GTTGTGATAA TAAATTTGGT TGTGCTTCAG TTTCAGTÒAC TACTGCTGGG TAGTTTTTAT

TTTGCATAAC TTCAGGGGGT ATTCCAGTTG GTGTTAGCAT TTGAAAGTCG AACTGCACTT 180

OGAATTTGGC TAC ATG GGA AAG ACA ATT CAG GTT TTC GĞA TTC CCT TAT 229 Met Gly Lys Thr Ile Gin Val Phe Gly Phe Pro Tyr 10

CTT CTC TCT GCG GAA GTG GTT AAG TCA TTC TTA GAG AAA TAT ACA GGA Leu Leu Ser Ala Glu Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly 15 20 25	277
TAT GGA ACT GTA TGT GCA TTG GAG GTT AAA CAG TCC AAA GGA GGA TCT Tyr Gly Thr Val Cys Als Leu Glu Val Lys Gln Ser Lys Gly Gly Ser 30 35 40	325
AGA GCA TTT GCC AAA GTT CAA TTT GCC GAC AAC ATA AGT GCT GAC AAA Arg Ala Phe Ala Lya Val Gln Phe Ala Asp Aan Ile Ser Ala Asp Lya 45 50 55 60	373
ATC ATC ACT TTG GCT AAT AAC AGG CTG TAT TIT GGC TCT TCT TAT TTG lle lle lle Thr Leu Ala Asn Asn Arg Leu Tyr Phe Gly Ser Sor Tyr Leu 65 70 75	421
AAG GCT TGG GAA ATG AAA ACT GAT ATT GTC CAA CTG CGG GCA TAT GTG Lys Ala Trp Glu Mot Lys Thr Asp Ile Val Gln Leu Arg Ala Tyr Val 80 85 90	469
GAT CAG ATG GAT GGC ATA ACT TTG AAT TTC GGA TGT CAG ATA TCA GAT Asp Gin Met Asp Gly Ile Thr Leu Asn Phe Gly Cys Gin Ile Ser Asp 95 100 105	517
GAC AAG TTT GCA GTG TTG GGA AGT ACA GAA GTT TCA ATT CAA TTT GGC Asp Lys Phe Ala Vai Leu Gly Ser Thr Ghu Vai Ser Ile Gln Phe Gly 110 115 120	565
ATT GGA TTG AAG AAA TTT TTT TTC TTT TTA TCT AGT GGT TCA GCT GAC Re Gly Leu Lys Lys Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp 125 130 135 140	613
TAT AAA CTT CAG CTT TCA TAT GAA AAT ATA TGG CAG GTT GTG CTC CAT Tyr Lys Leu Gln Leu Ser Tyr Glu Asn Ile Trp Gln Val Val Leu His 145 150 155	661
CGT CCA TAT GGT CAA AAT GCT CAG TTT CTC CTC ATA CAG TTA TIT GGT Arg Pro Tyr Gly Gin Aan Ala Gin Phe Lou Leu Ile Gin Leu Phe Gly 160 165 170	709
GCT CCT CGG ATC TAT AAG AGA CIT GAA AAC TCC TGT TAT AGC TTC TTT Ala Pro Arg Ile Tyr Lya Arg Leu Ghi Aan Ser Cys Tyr Ser Phe Phe 175 180 185	757
AAG GAA ACT CCT GAT GAT CAG TGG GTG AGG ACA ACA GAT TTC CCT CCA Lys Glu Thr Pro Asp Asp Gln Trp Val Arg Thr Thr Asp Phe Pro Pro 190 195 200	805
TCT TGG ATA GGG CTA TCT TCT AGC TTA TGT TTG CAG TTC CGT AGG GGT Ser Trp Ile Gly Leu Ser Ser Leu Cys Leu Gln Phe Arg Arg Gly 205 210 215 220	853
GTT CGT CTT CCA AAT TTC GAG GAA AGT TTT TTC CAC TAT GCA GAA CGT Val Arg Leu Pro Asm Phe Glu Glu Ser Phe Phe His Tyr Ala Glu Arg 225 230 235	901
GAA AAC AAT ATT ACT TTA CAG ACT GGT TTC ACC TTT TTC GTC TCT CAA Glu Asn Asn Ile Thr Leu Gln Thr Gly Phe Thr Phe Phe Val Ser Gln	949

AAA TCG GCT CTG GTT CCC AAT GTC CAG CCT CCG GAA GGA ATT TCA ATT 997 Lys Ser Ala Leu Val Pro Asn Val Gin Pro Pro Glu Gly Ile Ser Ile 255 - 260 265	
CCC TAC AAG ATT TTG TTC AAA ATT AGT TCT TTG GTA CAG CAT GGA TGC Pro Tyr Lys Ile Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys 270 275 280	
ATA CCT GGG CCA GCA TTA AAT GTC TAC TTT TTC CGA TTA GTT GAT CCT 1093 Le Pro Gly Pro Ala Leu Asn Val Tyr Phe Phe Arg Leu Val Asp Pro 285 290 295 300	
CGA AGG AGA AAT GTG GCA TGC ATT GAG CAT GCC TTA GAG AAA CTG TAC 114 Arg Arg Arg Asn Val Ala Cys IIe Glu His Ala Leu Ghu Lys Leu Tyr 305 310 315	1
TAT ATA AAG GAG TGC TGT TAT GAT CCC GTG AGG TGG CTC ACT GAG CAG Tyr Ile Lys Glu Cys Cys Tyr Asp Pro Val Arg Trp Leu Thr Glu Gln 320 325 330)
TAT GAT GGG TAT CTC AAG GGT AGA CAA CCT CCA AAA TCT CCG TCC ATC 1237 Tyr Asp Gly Tyr Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro Ser Ile 335 340 345	
ACT TTA GAT GAT GGG TTG GTG TAT GTA AGA AG	i
TGC AAA GTT TAT TTT TGT GGT CCA GAG GTT AAT GTT TCC AAT CGG GTT 1333 Cys Lys Val Tyr Phe Cys Gly Pro Glu Val Asn Val Ser Asn Arg Val 365 370 375 380	
CTC CGC AAT TAT TCT GAA GAC ATA GAT AAC TTT CTT CGT GTT TCT TTT 1381 Leu Arg Asn Tyr Ser Glu Asp Ile Asp Asn Phe Leu Arg Val Ser Phe 385 390 395	
OTT GAT GAG GAG TGG GAG AAA CTG TAT TCT ACA GAC TTA TTA CCA AAA 1429 Val Asp Glu Glu Trp Glu Lys Leu Tyr Ser Thr Asp Leu Leu Pro Lys 400 405 410)
GCA AGT ACT GGA AGT GGT GTC AGG ACA AAC ATC TAT GAG AGG ATC TTA Ala Ser Thr Gly Ser Gly Val Arg Thr Asn Ile Tyr Glu Arg Ile Leu 415 420 425	7
TCA ACT CTG CGG AAA GGC TTT GTA ATT GGT GAT AAA AAA TTT GAA TTT 1525 Ser Thr Leu Arg Lya Gly Phe Val Ile Gly Asp Lya Lya Phe Glu Phe 430 435 440	
CTT GCA TTT TCA TCG AGC CAG TTG CGG GAT AAT TCA GTG TGG ATG TTT Leu Ala Phe Ser Ser Gin Leu Arg Asp Asn Ser Val Trp Met Phe 450 450 450 1573	
GCA TCA AGA CCT GGC CTT ACT GCA AAT GAT ATA AGA GCT TGG ATG GGT Ala Ser Arg Pro Gly Leu Thr Ala Asa Asp Ile Arg Ala Trp Met Gly 465 470 475	

GAT TTT TCG CAG ATC AAG AAT GTC GCA AAA TAT GCT GCC AGA CTT GGT Asp Phe Ser Gin Ile Lys Asn Val Als Lys Tyr Als Als Arg Leu Gly 480 485 490	1669
CAA TCT TTT GGT TCC TCC AGA GAG ACT TTG AGT GTT CTT AGG CAT GAG Gln Ser Phe Gly Ser Ser Arg Ghu Thr Leu Ser Val Leu Arg His Ghu 495 500 505	1717
ATT GAA GTT ATT CCC GAT GTA AAG GTT CAT GGA ACC AGC TAT GTC TTT Ile Ghi Val Ile Pro Asp Val Lys Val His Gly Thr Ser Tyr Val Pho 510 515 520	1765
TCT GAT GGA ATT GGT AAA ATA TCT GGT GAC TTT GCT CAT AGA GTT GCC Ser Asp Gly Ile Gly Lys Ile Ser Gly Asp Phe Ala His Arg Val Ala 525 530 535 540	1813
TCA AAA TGT GGC CTT CAA TAT ACC CCA TCT GCT TTC CAG ATT CGT TAT Ser Lys Cys Gly Leu Gln Tyr Thr Pro Ser Ala Phe Gln Ile Arg Tyr 545 550 555	1861
GGT GGA TAT AAA GGT GTT GTG GGT GTT GAT CCG GAT TCA TCA ATG AAG Gly Gly Tyr Lys Gly Val Val Gly Val Asp Pro Asp Ser Ser Met Lys 560 565 570	1909
TTG TCT TTG AGA AAG AGC ATG TCG AAA TAT GAA TCA GAC AAC ATA AAG Leu Ser Leu Arg Lys Ser Met Ser Lys Tyr Glu Ser Asp Asn Ile Lys 575 580 585	1957
TTA GAT GTC CTT GGA TGG AGC AAA TAT CAG CCT TGT TAT CTT AAT CGT Leu Asp Val Leu Gly Trp Ser Lys Tyr Gln Pro Cys Tyr Leu Asn Arg 590 595 600	2005
CAA CTG ATT ACG CTC TTG TCT ACA CTT GGA GTG AAA GAT GAA GTT CTC Gin Leu Lie Thr Leu Leu Ser Thr Leu Gly Val Lys Aap Glu Val Leu 605 610 615 620	2053
GAA CAG AAG CAA AAG GAA GCT GTA GAT CAG CTT GAT GCT ATC TTG CAT Glu Gln Lys Gln Lys Glu Ala Val Asp Gln Leu Asp Ala Ile Leu His 625 630 635	2101
GAT TCT TTG AAG GCA CAG GAG GCT TTG GAA TTG ATG TCT CCT GGA GAG Asp Ser Leu Lys Ala Gln Glu Ala Leu Ghu Leu Met Ser Pro Gly Glu 640 645 650	2149
AAC ACT AAT ATT CTC AAG GCA ATG CTA AAC TGT GGT TAT AAG CCT GAT Asn Thr Asn Ile Leu Lys Ala Met Leu Asn Cys Gly Tyr Lys Pro Asp 655 660 665	2197
GCT GAG CCC TTT CTT TCA ATG ATG TTG CAA ACC TTC CGC GCA TCC AAG Ala Glu Pro Phe Leu Ser Met Met Leu Gln Thr Phe Arg Ala Ser Lys 670 675 680	2245
TTG CTC GAT TTG CGG ACT AGA TCA AGA ATA TTT ATT CCA AAT GGA AGA Leu Leu Asp Leu Arg Thr Arg Ser Arg Ile Phe Ile Pro Asn Gly Arg 685 690 695 700	2293
ACA ATG ATG GGA TGT TTG GAT GAA TCC AGA ACC TTG GAA TAT GGT CAG Thr Met Met Gly Cys Leu Asp Glu Ser Arg Thr Leu Glu Tyr Gly Gln	2341

705 710 7	715	
GTG TTT GTT CAG TTT ACT GGT C Val Phe Val Gin Phe Thr Gly Ala Gly F 720_ 725 730		2389
TTA CAT CCA TTT AAT AAC AGC A Leu His Pro Phe Asn Asn Ser Arg Ser T 735 740 745	AGA TCC ACC AAC AGT AAT TTC ATT CTG hr Aan Ser Asn Pho Ile Leu	2437
AAG GGA AAT GTG GTT GTT GCA Lys Gly Asm Val Val Val Ala Lys Asm F 750 755 760	AAA AAT CCA TGC TTG CAT CCT GGT GAT TO Cys Leu His Pro Gly Asp	2485
ATT CGT GTT TTA AAG GCT GTA A Ile Arg Vai Leu Lys Ala Vai Aan Vai Au 765 770 775	AAT GTT CGA GCG CTG CAC CAC ATG GTA rg Ala Leu His His Met Val 780	2533
Asp Cys Val Val Phe Pro Gh Lys Gly L	AA GGA AAA AGA CCT CAT CCG AAT GAA 198 Arg Pro His Pro Ass Glu 95	2581
TGT TCT GGG AGT GAT TTG GAT C Cys Ser Gly Ser Asp Leu Asp Gly Asp I 800 805 810	GGG GAT ATC TAC TTT GTT TGC TGG GAT le Tyr Phe Val Cys Trp Asp	2629
CAA GAC ATG ATC CCG CCA AGG Gin Asp Met Ile Pro Pro Arg Gin Val Gl 815 820 825	CAA GTC CAG CCG ATG GAA TAT CCT CCA II Pro Met Glu Tyr Pro Pro	2677
GCA CCC AGC ATA CAG TTG GAC C Ala Pro Ser Ile Gln Leu Asp His Asp Va 830 835 840	CAT GAT GTC ACA ATT GAG GAA GTT GAA I Thr Ile Ghu Glu Val Ghu	2725
GAG TAC TTC ACC AAC TAT ATT G Glu Tyr Phe Thr Asn Tyr Ile Vai Asn As 845 850 855	TG AAT GAC AGT TTG GGA ATC ATA GCA p Ser Leu Gly Ile Ile Ala 860	2773
AAT GCC CAT GTC GTA TTT GCA G Asn Ala His Val Val Phe Ala Asp Arg G 865 870 87		2821
GAT CCA TGC AAA AAA CTT GCT C Asp Pro Cys Lys Lys Leu Ala Glu Leu P 880 885 890	GAG CTC TTT TCA ATT GCA GTG GAC TTT ho Ser Ile Ala Val Asp Phe	2869
CCA AAG ACT GGT GTT CCC GCT G Pro Lys Thr Gly Val Pro Als Glu Ile Pro 895 900 905	PAA ATA CCA TCT CAG TTG CGC CCT AAA Ser Gin Leu Arg Pro Lys	2917
GAA TAC CCA GAC TTC ATG GAT A Glu Tyr Pro Asp Phe Met Asp Lys Pro A 910 915 920	AG CCG GAC AAG ACC AGC TAT ATC TCA sp Lys Thr Ser Tyr IIo Ser	2965
GAA AGA GTT ATT GGA AAG CTT T Glu Arg Val Ile Gly Lya Leu Phe Arg Ly 925 930 935	TTC AGG AAA GTG AAG GAC AAA GCA CCT 8 Val Lys Asp Lys Ala Pro 940	3013

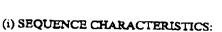
CAG GCT AGC TCT ATC GCG ACC TTC ACA AGA GAT GTT GCA AGG AGA TCA	304
Gln Ala Ser Ser Ile Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser 945 950 955	3061
TAT GAT GCT GAT ATG GAA GTT GAT GGA TTT GAA GAT TAC ATT GAC GAA Tyr Asp Ala Asp Met Glu Val Asp Gly Phe Glu Asp Tyr Ile Asp Glu 960 965 970	3109
GCT TTT GAC TAC AAA ACT GAA TAT GAC AAC AAG CTG GGT AAT TTA ATG Als Phe Asp Tyr Lys Thr Ghu Tyr Asp Asn Lys Leu Gly Asn Leu Met 975 980 985	3157
GAC TAC TAT GGC ATA AAA ACA GAG GCT GAA ATA CTT AGT GGT GGC ATT Asp Tyr Tyr Gly Ile Lys Thr Glu Ala Glu Ile Leu Ser Gly Gly Ile 990 995 1000	3205
ATG AAG GCA TCA AAA ACT TTT GAC CGC AGA AAA GAT GCT GAG GCC ATT Met Lys Ala Ser Lys Thr Phe Asp Arg Arg Lys Asp Ala Glu Ala Ile 1005 1010 1015 1020	3253
AGT GTT GCT GTG AGG GCC TTG AGG AAG GAG GCA AGA GCC TGG TTC AAG Ser Val Ala Val Arg Ala Leu Arg Lys Glu Ala Arg Ala Trp Phe Lys 1025 1030 1035	3301
AGG CGT AAT GAT ATA GAT GAC ATG TTA CCA AAG GCT TCG GCT TGG TAC Arg Arg Asn Asp Ile Asp Asp Met Leu Pro Lys Ala Ser Ala Trp Tyr 1040 1045 1050	3349
CAC GTT ACA TAT CAT CCT ACA TAT TGG GGT TGC TAC AAT CAG GGG TTG His Val Thr Tyr His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly Leu 1055 1060 1065	3397
AAA AGA GCT CAT TTC ATT AGC TTT CCC TGG TGT GTT TAT GAC CAG CTA Lys Arg Ala His Phe He Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu 1070 1075 1080	3445
ATC CAG ATT AAG AAG GAC AAA GCA CGT AAC AGG CCA GTT CTC AAC TTG lle Gin lie Lys Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu 1085 1090 1095 1100	3493
TCA TCT CTC AGG GCT CAA CTG AGT CAC AGA TTA GTG TTG AAA Ser Ser Leu Arg Ala Gin Leu Ser His Arg Leu Val Leu Lys 1105 1110	•
TGAGATTCCA GTCGAGCGTT AAGCTGATAT ATATATAATG TAATAGGGTG TGATCATAAG 3595	
AAAACTGTTA TGCATTGTTG ACTACCTTTT GTCTTTAAAA CTGCATGAAG CTGC. 3655	AACATA

TATGCAGTAC TCTAAGAAAC AGATGTACAG CTAAGTACTA ATATGTATGT GATTTGAGTT 3715

TCATCTTTCT TCTAAA

3731

(2) INFORMATION FOR SEQ ID NO: 2:



- (A) LENGTH: 1114 amino acida
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Gly Lya Thr Ile Gln Val Phe Gly Phe Pro Tyr Leu Leu Ser Ala 1 5 10 15

Ghu Val Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly Tyr Gly Thr Val 20 25 30

Cys Ala Leu Glu Val Lys Gln Ser Lys Gly Gly Ser Arg Ala Phe Ala 35 40 45

Lys Val Gin Phe Ala Asp Asn Ile Ser Ala Asp Lys Ile Ile Thr Leu 50 55 60

Ala Asn Asn Arg Leu Tyr Phe Gly Ser Ser Tyr Leu Lys Ala Trp Glu 65 70 75 80

Met Lys Thr Asp Re Val Gin Leu Arg Ala Tyr Val Asp Gin Met Asp 85 90 95

Gly No Thr Leu Asn Pho Gly Cys Gln No Ser Asp Asp Lys Pho Ala 100 105 110

Val Leu Gly Ser Thr Glu Val Ser Ile Gln Phe Gly Ile Gly Leu Lys 115 120 125

Lys Phe Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp Tyr Lys Leu Gln 130 135 140

Leu Ser Tyr Glu Aan Ile Trp Gln Val Val Leu His Arg Pro Tyr Gly
145 150 155 160

Gln Asn Ala Gln Phe Leu Leu Ile Gln Leu Phe Gly Ala Pro Arg Ile 165 170 175

Tyr Lys Arg Leu Glu Asn Ser Cys Tyr Ser Phe Phe Lys Glu Thr Pro 180 185 190

Asp Asp Gin Trp Val Arg Thr Thr Asp Phe Pro Pro Ser Trp Ile Gly 195 200 205

Leu Ser Ser Ser Leu Cys Leu Gh Phe Arg Arg Gly Val Arg Leu Pro 210 215 220

Asn Phe Glu Ghu Ser Phe Phe His Tyr Ala Glu Arg Glu Asn Asn Ile 225 230 235 240

Thr Leu Gin Thr Gly Phe Thr Phe Phe Val Ser Gin Lys Ser Ala Leu 245 250 255

Val Pro Asn Val Gin Pro Pro Glu Gly Ile Ser Ile Pro Tyr Lys Ile 260 265 270

- Leu Pho Lys Ile Ser Ser Leu Val Gln His Gly Cys Ile Pro Gly Pro 275 280 285
- Ala Leu Asn Val Tyr Phe Phe Arg Leu Val Asp Pro Arg Arg Arg Asn 290 295 300
- Val Ala Cys Ile Glu His Ala Leu Glu Lys Leu Tyr Tyr Ile Lys Glu 305 310 315 320
- Cys Cys Tyr Asp Pro Val Arg Trp Leu Thr Glu Gln Tyr Asp Gly Tyr 325 330 335
- Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro Ser Ile Thr Leu Asp Asp 340 345 350
- Gly Leu Val Tyr Val Arg Arg Val Leu Val Thr Pro Cys Lys Val Tyr 355 360 365
- Phe Cys Gly Pro Glu Val Asn Val Ser Asn Arg Val Leu Arg Asn Tyr 370 375 380
- Ser Glu Asp IIe Asp Asn Phe Leu Arg Val Ser Phe Val Asp Glu Glu 385 390 395 400
- Trp Glu Lys Leu Tyr Ser Thr Asp Leu Leu Pro Lys Ala Ser Thr Gly
 405 410 415
- Ser Gly Val Arg Thr Aan Ile Tyr Glu Arg Ile Leu Ser Thr Leu Arg 420 425 430
- Lys Gly Phe Val Ile Gly Asp Lys Lys Phe Ghi Phe Leu Ala Phe Ser 435 440 445
- Ser Ser Gln Leu Arg Asp Asn Ser Val Trp Met Phe Ala Ser Arg Pro 450 455 460
- Gly Leu Thr Aia Asn Asp Ile Arg Ala Trp Met Gly Asp Phe Ser Gln 465 470 475 480
- Ile Lys Asn Val Ala Lys Tyr Ala Ala Arg Leu Gly Gin Ser Phe Gly
 485 490 495
- Ser Ser Arg Glu Thr Leu Ser Val Leu Arg His Glu Ile Glu Val Ile 500 505 510
- Pro Asp Val Lys Val His Gly Thr Ser Tyr Val Phe Ser Asp Gly lle 515 520 525
- Gly Lys IIe Ser Gly Asp Phe Ala His Arg Val Ala Ser Lys Cys Gly 530 535 540
- Leu Gin Tyr Thr Pro Ser Ala Phe Gin Ile Arg Tyr Gly Gly Tyr Lys 545 550 555 560
- Gly Val Val Gly Val Asp Pro Asp Ser Ser Met Lys Leu Ser Leu Arg 565 570 575

- Lys Ser Met Ser Lys Tyr Ghı Ser Asp Asn Ile Lys Leu Asp Val Leu 580 585 590
- Gly Trp Ser Lys Tyr Gln Pro Cys Tyr Leu Asn Arg Gln Leu Ile Thr 595 - 600 605
- Leu Leu Ser Thr Leu Gly Val Lys Asp Glu Val Leu Glu Gln Lys Gln 610 615 620
- Lys Ghu Ala Val Asp Gln Leu Asp Ala Ile Leu His Asp Ser Leu Lys 625 630 635 640
- Ala Glu Ala Leu Glu Leu Met Ser Pro Gly Glu Asn Thr Asn Ile 645 650 655
- Leu Lys Ala Met Leu Asn Cys Gly Tyr Lys Pro Asp Ala Glu Pro Phe 660 665 670
- Leu Ser Met Met Leu Gin Thr Phe Arg Ala Ser Lya Leu Leu Asp Leu 675 680 685
- Arg Thr Arg Ser Arg Ile Phe Ile Pro Asn Gly Arg Thr Met Met Gly 690 695 700
- Cys Leu Asp Glu Ser Arg Thr Leu Glu Tyr Gly Gln Val Phe Val Gln 705 710 715 720
- Phe Thr Gly Ala Gly His Gly Glu Phe Ser Asp Asp Leu His Pro Phe 725 730 735
- Asn Asn Ser Arg Ser Thr Asn Ser Asn Phe Ile Leu Lys Gly Asn Val 740 745 750
- Val Val Ala Lys Asn Pro Cys Leu His Pro Gly Asp Re Arg Val Leu 755 760 765
- Lys Ala Val Asn Val Arg Ala Leu His His Met Val Asp Cys Val Val 770 775 780
- Phe Pro Gln Lys Gly Lys Arg Pro His Pro Asn Glu Cys Ser Gly Ser 785 790 795 800
- Asp Leu Asp Gly Asp Re Tyr Phe Val Cys Trp Asp Gln Asp Met Re 805 810 815
- Pro Pro Arg Gln Val Gln Pro Met Glu Tyr Pro Pro Ala Pro Ser Ile 820 825 830
- Gln Leu Asp His Asp Val Thr Ile Glu Glu Val Glu Glu Tyr Phe Thr 835 840 845
- Asn Tyr Ile Val Asn Asp Ser Leu Gly Ile Ile Ala Asn Ala His Val 850 855 860
- Val Phe Ala Asp Arg Glu Pro Asp Met Ala Met Ser Asp Pro Cys Lys 865 870 875 880
- Lys Leu Ala Glu Leu Phe Ser Ile Ala Val Asp Phe Pro Lys Thr Gly

l.

885

890

895

Val Pro Ala Glu Ile Pro Ser Gln Leu Arg Pro Lys Ghu Tyr Pro Asp 900 905 910

Phe Met Asp Lys Pro Asp Lys Thr Ser Tyr Ile Ser Glu Arg Val Ile
915
920
925

Gly Lys Lou Phe Arg Lys Val Lys Asp Lys Ala Pro Gin Ala Ser Ser 930 935 940

Ile Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser Tyr Asp Ala Asp 945 950 955 960

Mot Glu Val Asp Gly Phe Glu Asp Tyr Ile Asp Glu Ala Phe Asp Tyr
965 970 975

Lys Thr Glu Tyr Asp Asn Lys Leu Gly Asn Leu Met Asp Tyr Tyr Gly 980 985 990

The Lys Thr Glu Ala Ghu He Leu Ser Gly Gly He Met Lys Ala Ser 995 1000 1005

Lys Thr Phe Asp Arg Arg Lys Asp Ala Ghu Ala Ile Ser Val Ala Val 1010 1015 1020

Arg Ala Leu Arg Lys Glu Ala Arg Ala Tro Phe Lys Arg Arg Asn Asp 1025 1030 1035 1040

Ile Asp Asp Met Leu Pro Lys Ala Ser Ala Trp Tyr His Val Thr Tyr 1045 1050 1055

His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly Let Lys Arg Ala His 1060 1065 1070

Phe Re Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu Re Gin He Lys 1075 1080 1085

Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu Ser Ser Leu Arg 1090 1095 1100

Ala Gln Leu Ser His Arg Leu Val Leu Lya 1105 1110